

Fig. 1

Ala	Pro	Pro	Arg	Leu	Ile	Cys	Asp	Ser	Arg	Val	Leu	Glu	Arg	Tyr	Leu
1					5					10					15
Leu	Glu	Ala	Lys	Glu	Ala	Glu	Asn	Ile	Thr	Thr	Gly	Cys	Ala	Glu	His
			20					25					30		
Cys	Ser	Leu	Asn	Glu	Asn	Ile	Thr	Val	Pro	Asp	Thr	Lys	Val	Asn	Phe
		35					40					45			
Tyr	Ala	Trp	Lys	Arg	Met	Glu	Val	Gly	Gln	Gln	Ala	Val	Glu	Val	Trp
	50					55					60				
Gln	Gly	Leu	Ala	Leu	Leu	Ser	Glu	Ala	Val	Leu	Arg	Gly	Gln	Ala	Leu
65					70					75				80	
Leu	Val	Asn	Ser	Ser	Gln	Pro	Trp	Glu	Pro	Leu	Gln	Leu	His	Val	Asp
				85					90					95	
Lys	Ala	Val	Ser	Gly	Leu	Arg	Ser	Leu	Thr	Thr	Leu	Leu	Arg	Ala	Leu
			100					105					110		
Gly	Ala	Gln	Lys	Glu	Ala	Ile	Ser	Pro	Pro	Asp	Ala	Ala	Ser	Ala	Ala
	115						120					125			
Pro	Leu	Arg	Thr	Ile	Thr	Ala	Asp	Thr	Phe	Arg	Lys	Leu	Phe	Arg	Val
	130					135					140				
Tyr	Ser	Asn	Phe	Leu	Arg	Gly	Lys	Leu	Lys	Leu	Tyr	Thr	Gly	Glu	Ala
145				150				155						160	
Cys	Arg	Thr	Gly	Asp											
				165											

Fig. 2

Ala	Pro	Pro	Arg	Leu	Ile	Cys	Asp	Ser	Arg	Val	Leu	Glu	Arg	Tyr	Leu
1				5				10						15	
Leu	Glu	Ala	Lys	Glu	Ala	Glu	Asn	Ile	Thr	Thr	Gly	Cys	Ala	Glu	His
			20					25						30	
Cys	Ser	Leu	Asn	Glu	Asn	Ile	Thr	Val	Pro	Asp	Thr	Lys	Val	Asn	Phe
		35					40					45			
Tyr	Ala	Trp	Lys	Arg	Met	Glu	Val	Gly	Gln	Gln	Ala	Val	Glu	Val	Trp
	50					55					60				
Gln	Gly	Leu	Ala	Leu	Leu	Ser	Glu	Ala	Val	Leu	Arg	Gly	Gln	Ala	Leu
65					70					75				80	
Leu	Val	Asn	Ser	Ser	Gln	Pro	Trp	Glu	Pro	Leu	Gln	Leu	His	Val	Asp
				85					90					95	
Lys	Ala	Val	Ser	Gly	Leu	Arg	Ser	Leu	Thr	Thr	Leu	Leu	Arg	Ala	Leu
			100					105						110	
Gly	Ala	Gln	Lys	Glu	Ala	Ile	Ser	Pro	Pro	Asp	Ala	Ala	Ser	Ala	Ala
	115						120						125		
Pro	Leu	Arg	Thr	Ile	Thr	Ala	Asp	Thr	Phe	Arg	Lys	Leu	Phe	Arg	Val
	130					135						140			
Tyr	Ser	Asn	Phe	Leu	Arg	Gly	Lys	Leu	Lys	Leu	Tyr	Thr	Gly	Glu	Ala
145				150						155				160	
Cys	Arg	Thr	Gly	Asp	Arg										
				165											

Fig. 3

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GGAATTCACCAACATGGGGGTGCACGAATGTCCTGCCTGGCTGTGGCTTCTCCTGTCCCT
1  -----+-----+-----+-----+-----+-----+ 60
CCTTAAGTGGTGGTACCCCACTGCTTACAGGACGGACCGACCCGAAGAGGACAGGGA
      M G V H E C P A W L W L L L S L -

GCTGTCGCTCCCTCTGGGCCTCCCACTCCTGGGCGCCCCCCCCGAATCAGAGGCCGCGC
61  -----+-----+-----+-----+-----+-----+ 120
CGACAGCGAGGGAGACCCGGAGGGTCAGGACCCGCGGGGGGGGCTTAGCTCCCGCGCG
      L S L P L G L P V L G A P P R I E G R A -

CCCCACAGCCTCATCTGTGACAGCCGAGTCCTGGAGAGGTACCTCTTGGAGGCCAAGGA
121 -----+-----+-----+-----+-----+-----+ 180
GGTGGTGCGGAGTAGACACTGTCGGCTCAGGACCTCTCCATGGAGAACCTCCGGTTCCT
      P P R L I C D S R V L E R Y L L E A K E -

GGCCGAGAATATCACGACGGGCTGTGCTGAACACTGCAGCTTGAATGAGAATATCACTGT
181 -----+-----+-----+-----+-----+-----+ 240
CCGGCTCTTATAGTGCTGCCCGACACGACTTGTGACGTCGAACCTTACTCTTATAGTGACA
      A E N I T T G C A E H C S L N E N I T V -

CCAGACACCAAAGTTAATTTCTATGCCTGGAAGAGATGGAGGTCGGGCAGCAGGCCGT
241 -----+-----+-----+-----+-----+-----+ 300
GGGCTGTGTTTCAATTAAGATACGGACCTTCTCTACCTCCAGCCGTCGTCGGCA
      P D T K V N F Y A W K R M E V G Q Q A V -

AGAAGTCTGGCAGGGCTGGCCCTGCTGTCGAAGCTGTCTGCGGGCCAGGCCCTGTT
301 -----+-----+-----+-----+-----+-----+ 360
TCTTCAGACGTCCTCCGACCGGACGACAGCCTTCGACAGGACGCCCGGTCCGGGACAA
      E V W Q G L A L L S E A V L R G Q A L L -

GGTCAACTCTTCCAGCCGTGGGAGCCCTGCAGCTGCATGTGGATAAAGCCGTCACTGG
361 -----+-----+-----+-----+-----+-----+ 420
CCAGTTGAGAAAGGTCGGCACCTCGGGGACGTCGACGTACACCTATTTTCGGCAGTACC
      V N S S Q P W E P L Q L H V D K A V S G -

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CCTTCGCAGCCTCACCACCTCTGCTTCGGGCTCTGGGAGCCCAGAAGGAAGCCATCTCCCC
 421 -----+-----+-----+-----+-----+ 480
 GGAAGCGTCGGAGTGGTGAGACGAAGCCGAGACCTCGGGTCTTCCTTCGGTAGAGGGG
 L R S L T T L L R A L G A Q K E A I S P -

TCCAGATGCGCCTCAGCTGCTCCACTCCGAACAATCACTGCTGACACTTTCGCAAAC
 481 -----+-----+-----+-----+-----+ 540
 AGGTCTACGCCGGAGTCGACGAGGTGAGGCTTGTTAGTGACACTGTGAAAGGCGTTTGA
 P D A A S A A P L R T I T A D T F R K L -

CTTCGAGTCTACTCCAATTTCTCCGGGAAAGCTGAAGCTGTACACAGGGGAGGCGTG
 541 -----+-----+-----+-----+-----+ 600
 GAAGGCTCAGATGAGGTAAAGGAGGCCCTTTGACTTCGACATGTGTCCTCCCGGAC
 F R V Y S N F L R G K L K L Y T G E A C -

CAGGACAGGGGACAGATGACCAGGTCGAC
 601 -----+-----+-----+-----+ 629
 GTCTGTCCCTGTCTACTGGTCCAGCTG
 R T G D R * -

Fig. 4

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GGAATTCACCAACCATGGGGTGCACGAATGCTCTGCCTGGCTGTGGCTTCTCTGTCCT
1  -----+-----+-----+-----+-----+ 60
CCTTAAGTGGTGTACCCACGTGCTTACAGGACGACCGACCGAAGAGGACAGGGA
        M  G  V  H  E  C  P  A  W  L  W  L  L  L  S  L  -

GCTGTCGCTCCCTCTGGGCTCCAGTCCTGGGCGCCCCCGCCCCACGACGCTCAT
61  -----+-----+-----+-----+-----+ 120
CGACAGCGAGGGAGACCCGGAGGGTCAGGACCCGCGGGGGGGCGGGGTGGTGCAGGTA
  L  S  L  P  L  G  L  P  V  L  G  A  P  P  A  P  R  L  I  -

CTGTGACAGCCGAGTCTGGAGAGGTACCTCTTGGAGGCCAAGGAGCCGAGAATATCAC
121 -----+-----+-----+-----+-----+ 180
GACACTGTCGGCTCAGGACCTCTCCATGGAGAACCTCCGGTTCCTCGGCTCTTATAGTG
      C  D  S  R  V  L  E  R  Y  L  L  E  A  K  E  A  E  N  I  T  -

GACGGGTGTGTGAACACTGCAGCTTGAATGAGAATATCACTGTCCAGACACCAAAGT
181 -----+-----+-----+-----+-----+ 240
CTGCCCCGACGACTTGTGACGTCGAACCTACTCTTATAGTGACAGGGTCTGTGGTTTCA
      T  G  C  A  E  H  C  S  L  N  E  N  I  T  V  P  D  T  K  V  -

TAATTTCTATGCCGGAAGAGGATGGAGGTGCGGCGAGGCGCTAGAAGTCTGGCAGGG
241 -----+-----+-----+-----+-----+ 300
ATTAAGATACGGACCTTCTCCTACCTCCAGCCGTCGTCCGGCATCTTCAGACCTGCC
      N  F  Y  A  W  K  R  M  E  V  G  Q  Q  A  V  E  V  W  Q  G  -

CCTGGCCCTGCTGTGGAAGCTGTCTGCGGGGCCAGGCCCTGTTGTCAACTCTTCCCA
301 -----+-----+-----+-----+-----+ 360
GGACCGGGACGACGCTTCGACAGGACGCCCGGTCCGGGACAACAGTTGAGAAGGGT
      L  A  L  L  S  E  A  V  L  R  G  Q  A  L  L  V  N  S  S  Q  -

GCCGTGGGAGCCCTGCAGCTGCATGTGGATAAAGCCGTGAGTGGCCTTCGACGCTCAC
361 -----+-----+-----+-----+-----+ 420
CGGCACCTTCGGGGACGTCGACGTACACCTATTTGCGCAGTCACCGGAAGCGTCGAGTG
      P  W  E  P  L  Q  L  H  V  D  K  A  V  S  G  L  R  S  L  T  -

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CACTCTGCTTCGGGCTCTGGGAGCCCAGAAGGAAGCCATCTCCCTCCAGATGCGGCCTC
 421 -----+-----+-----+-----+-----+ 480
 GTGAGACGAAGCCCAGACCTCGGGTCTTCCTTCGGTAGAGGGGAGGTCTACGCCGGAG
 T L L R A L G A Q K E A I S P P D A A S -

AGCTGCTCCACTCCGAACAATCACTGCTGACACTTTCGCCAAACTCTTCGAGTCTACTC
 481 -----+-----+-----+-----+-----+ 540
 TCGACGAGGTGAGGCTTGTTAGTGACGACTGTGAAAGGC GTTTGAGAAGGCTCAGATGAG
 A A P L R T I T A D T F R K L F R V Y S -

CAATTTCTCCGGGAAAGCTGAAGCTGTACACAGGGGAGGCTGCAGGACAGGGGACAG
 541 -----+-----+-----+-----+-----+ 600
 GTTAAAGGAGGCCCTTTGACTTCGACATGTGTCCTCCGGACGTCCTGTCCCTGTC
 N F L R G K L K L Y T G E A C R T G D R -

ATGACCAAGGTCGAC
 601 -----+----- 614
 TACTGGTCCAGCTG
 * -

Fig. 5

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GGAATTACCACCATGGGGTGCACGAATGTCCTGCCTGGCTGTGGCTTCTCTGTCCCT
1  -----+-----+-----+-----+-----+ 60
CCTTAAGTGGTGTACCCCACTGCTTACAGGACGGACCGACCCGAAGAGGACAGGGA
        M  G  V  H  E  C  P  A  W  L  W  L  L  L  S  L  -

GCTGTCGCTCCCTCTGGGCTCCCACTGCTGGGCGCCCCCGGCGCCGCCACTACGC
61  -----+-----+-----+-----+-----+ 120
CGACAGCGAGGGAGACCCGGAGGTACAGGACCCGCGGGGGGGCCGCGCGGGTGATGCG
  L  S  L  P  L  G  L  P  V  L  G  A  P  P  G  A  A  H  Y  A  -

CCACCAACGCTCATCTGTGACAGCCGAGTCTGGAGAGGTACCTCTTGGAGGCCAAGGA
121 -----+-----+-----+-----+-----+ 180
GGGTGGTGGGAGTAGACACTGTCGGCTCAGGACCTCTCCATGGAGAACCTCCGGTTCCT
      P  P  R  L  I  C  D  S  R  V  L  E  R  Y  L  L  E  A  K  E  -

GGCCGAGAATATCACACGGGCTGTGCTGAACACTGCAGCTTGAATGAGAATATACTGT
181 -----+-----+-----+-----+-----+ 240
CCGGCTCTTATAGTGCTGCCGACACGACTTGTGACGTGCAACTTACTCTTATAGTGACA
      A  E  N  I  T  T  G  C  A  E  H  C  S  L  N  E  N  I  T  V  -

CCACAGACACAAAGTTAATTTCTATGCCTGGAAGAGGATGGAGGTCGGGACAGCGCCGT
241 -----+-----+-----+-----+-----+ 300
GGGTCTGTGGTTTCAATTAAGATACGGACCTTCTCTACCTCCAGCCGTCGTCCGGCA
      P  D  T  K  V  N  F  Y  A  W  K  R  M  E  V  G  Q  Q  A  V  -

AGAACTCTGGCAGGGCTGGCCCTGCTGTCGGAAGCTGTCTGCGGGGCCAGGCCCTGTT
301 -----+-----+-----+-----+-----+ 360
TCTTCAGACCGTCCCGACCGGGACGACAGCCTTCGACAGGACGCCCGGTCCGGGACAA
      E  V  W  Q  G  L  A  L  L  S  E  A  V  L  R  G  Q  A  L  L  -

GGTCAACTCTTCCAGCCGTGGGAGCCCTGCAGCTGCATGTGGATAAAGCCGTCAGTGG
361 -----+-----+-----+-----+-----+ 420
CCAGTTGAGAAGGGTCGGCACCTCGGGACGTCGACGTACACCTATTTCCGCGAGTCACC
      V  N  S  S  Q  P  W  E  P  L  Q  L  H  V  D  K  A  V  S  G  -

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CCTTCGCAGCCTCACCCTCTGCTTCGGGCTCTGGGAGCCAGAAGGAAGCCATCTCCCC
 421 -----+-----+-----+-----+-----+ 480
 GGAAGCGTCGGAGTGGTGAGACGAAGCCCAGACCTCGGGTCTTCCTTCGGTAGAGGGG
 L R S L T T L L R A L G A Q K E A I S P -

 TCCAGATGCGGCCTCAGCTGCTCCACTCCGAACAATCACTGCTGACACTTTCGCAAACT
 481 -----+-----+-----+-----+-----+ 540
 AGGTCTACGCCGGAGTCGACGAGGTGAGGCTTGTTAGTGACGACTGTGAAAGGC GTTGA
 P D A A S A A P L R T I T A D T F R K L -

 CTTCGAGTCTACTCCAATTTCTCCGGGGAAAGCTGAAGCTGTACAGGGGAGGCCTG
 541 -----+-----+-----+-----+-----+ 600
 GAAGGCTCAGATGAGGTTAAAGGAGGCCCTTCGACTTCGACATGTGYCCCTCCGGAC
 F R V Y S N F L R G K L K L Y T G E A C -

 CAAGACAGGGGACAGATGACCAGGTCGAC
 601 -----+-----+-----+-----+ 629
 GTCTGTCCCTGTCTACTGGTCCAGCTG
 R T G D R * -